

Attorney's Docket No.: 10287-043001 / MGH 1286.0

Airda  
10/17/00

## IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant : Katia Georgopoulos et al.  
Serial No. : 09/259,389  
Filed : February 26, 1999  
Title : THE HELIOS GENE

Art Unit : 1632  
Examiner : Joseph Woitach

Commissioner for Patents  
Washington, D.C. 20231

DECLARATION OF KATIA GEORGOPOULOS UNDER 37 C.F.R. §1.131

I, Katia Georgopoulos, declare as follows:

1. I am an inventor on the above-captioned patent application.

2. The claimed nucleic acid invention was first conceived and reduced to practice in the United States by the inventors prior to February 4, 1998, the publication date of Hahm et al. (GenBank™ Accession Number AF044257). Attached as Exhibit A is a true copy of a record which reports experiments setting forth the nucleotide sequence of a murine Helios cDNA. The date of the sequence analysis of Exhibit A, which is obscured in this copy as permitted by the Manual of Patent Examining Procedure § 715.07, is prior to February 4, 1998.

3. I further declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of this application or any patent issuing thereon.

09/27/00  
Date

Katia Georgopoulos

20128501.doc

## CERTIFICATE OF MAILING BY FIRST CLASS MAIL

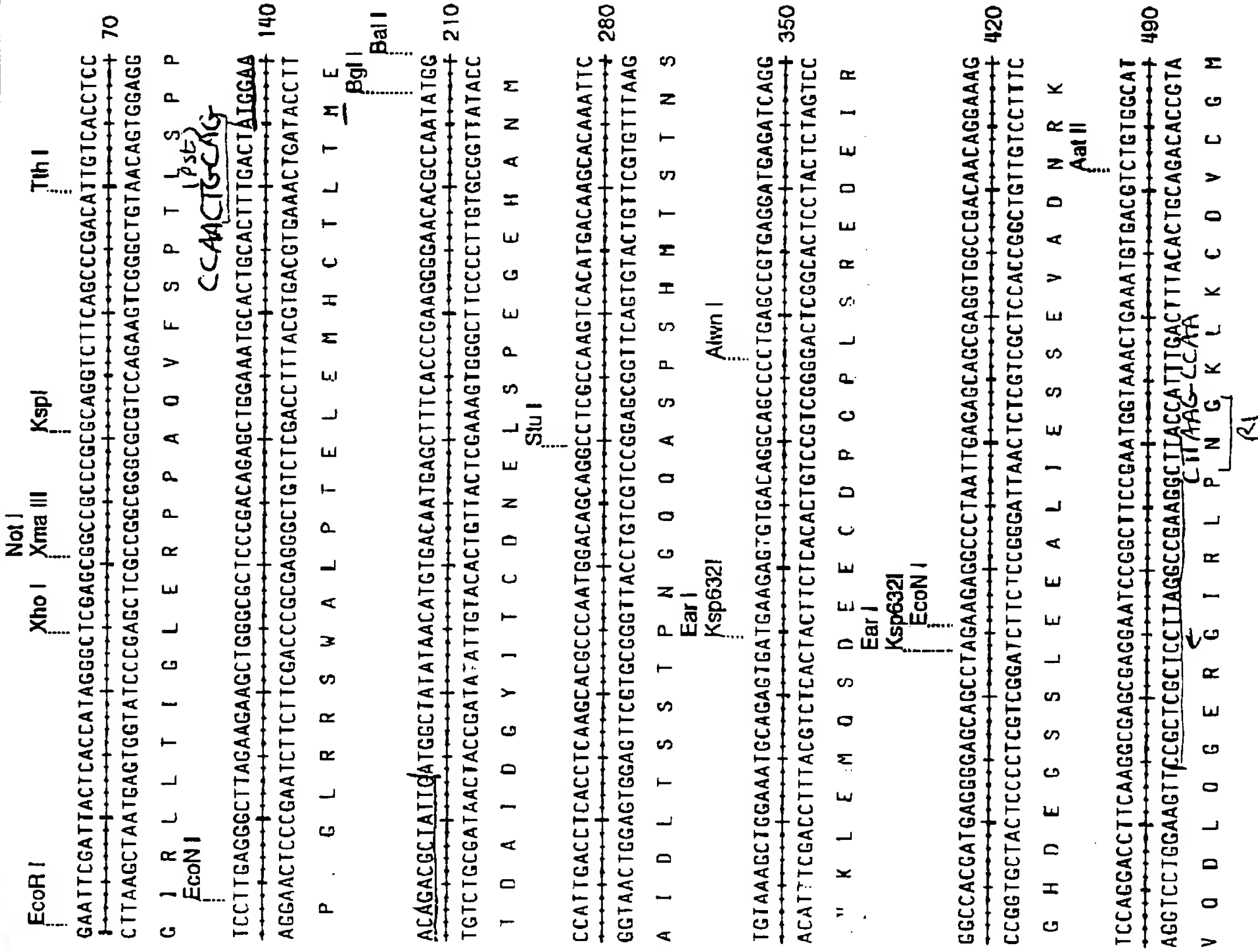
I hereby certify under 37 CFR §1.8(a) that this correspondence is being deposited with the United States Postal Service as first class mail with sufficient postage on the date indicated below and is addressed to the Commissioner for Patents, Washington, D.C. 20231.

September 29, 2000  
Date of Deposit  
  
Signature  
Lisa G. Gray  
Typed or Printed Name of Person Signing Certificate

mHeliosCod Map (1 > 1732) Site and Sequence

Enzymes: 70 of 146 enzymes (Filtered)

Settings: Linear, Certain Sites Only, Standard Genetic Code



- 1) 325 bp frag → amplify by PCR
- 2) digest PCR frag and vector with Pst and EcoRI
- 3) Run on gel; purify from gel slice
- 4) ligate
- 5) transform bupp. + determine which has correct clone
- 6) pick colonies

460  
155  
225

mHeliosCod Map (1 > 1732) Site and Sequence

GGTTTGCATIGGGCCCAATGIGCTTATGGTACATAAAAGGAGTCACACIGGTGAGCGGCCCTTCCACTGT 560  
CCAAACGTAAACCCGGTTACACGAATACCAATGATATTTCCICAGTGTGACCACTGCCCGGAAGGTGACA  
V C I G P N V L M V H K R S H T G E R P F H C  
AACCAGTCCGGACGTTCTTTTACCAGAAAGGCMACCTTCTGAGACACATAAAGTTACRCKYTGGRGARA  
630  
TTGGTCACGCCICGCAAGAAAATGGGCTCTCCCGKTGGAAGACTCTGTGTAATTTCAATGYGMRACCYCTYT  
N O C G R S F T O K G ? L L R H I K L ? ? G E  
OxaNI  
AGCCSTTCAAATGICCTTCTGIGTAGCTATGCTIIGTAGAAGAAGGACGCTCTCACAGGACACCTCAGGAC  
700  
TCGSAAGTTTACAGGAAGACATCGATACGAACATCTTCTTCCICGAGAGTGCTCTGTGGAGTCCTG  
K P F K C P F C S Y A C R R R D A L T G H L R T  
PIM I  
CCATTCTGTGGGTAAACCTCACAAAGTGTAACTACTGTGGCGAAGCTACAAGCAGCGCACGTCACCTGGAG  
770  
GGTAAGACACCCCATTTGGAGTGTTCACATTGATGACACCGGCTTCGATGTTCTGTCGCGTGCAGTGACCTC  
H S V G K P H K C C N Y C G R S Y K O R T S L E  
BspHI  
GAACACAAGGAACGCIGTCACAACTATCTCCAGAAATGTGAGGAGGCTGCGGGCAGGTGATGAGTC 840  
CITGTGTTCCCTTGGACAGTGTGATAGAGGTCTTACAGTCGTACCTCCGACGGCCCGTCCAGTACTCAG  
E H K E R C H N Y L O N V S M E A A G Q V M S  
SspI  
ACCATGTACCGCCTATGGAAGATTGTAAAGGAACAAGAGCCTATCATGGACAACAATATTTCTCTGGTGC 910  
TGGTACATGCGGATACCTTCTAACATTCTTGTCTCGGATAGTACCTGTTGTTATAAGAGACCAACG  
H H V P P M E D C K E Q E P I M D N N I S L V A  
TTTGGAGAGACCTGCTGTATAGAGAAGCTCAGCGGAAATATGGBAAGCCAAAGCTCCACCTCCTCAG  
980  
AAACTCTCTGGACGACAGTATCTCTCGAGTCCGCTTATACCCCTTCCGCTTTCGAGGTGAGGAGTC  
F E R P A V I E K L T A N M G K R K S S T P Q  
HindIII  
AAGTTTGTGGGGAAAGCTTATGCGATTTCAGTACCCAGATATTCATTTTCATAIGAACCTTAACATATG 1050  
TTCAACACACCCCTTTTCGAATACGTAAGTCGATGGGTCTATAAGTAAAGTATATCTGAATTGTATAC  
K F V G E K L M R F S Y P D I H F H M N L T Y  
EspI  
AGAAGGAGGCTGAGCTGATGCGTCTCATATGATGGACCAAGCCATCAACAATGCAATCACCTACCTTGG 1120  
TCTTCTCCGACTCGACTACGTCAGAGTACTACTCGTTCGGTAGTTGTTACGTTAGTGGAACCC  
E K E A E L M O S H M M D O A I N N A I T Y L G

### Site and Sequence

[illegible]